

Reconsidered 1/9/07 187

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 17, 2003, 09:13:37 ; Search time 3691 Seconds
(without alignments)
10496.184 Million cell updates/sec.

Title: US-10-043-539A-1
Perfect score: 947
Sequence: 1 gtttcaaatcggtggagg.....gtttcaaatcgatgatcat 947

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 288711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sts.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rat.*
- 36: em.htg.sam.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.higo.hum.*
- 40: em.higo.mus.*
- 41: em.higo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	947	1	AF207701 Staphyloc
C 2	826.4	87.3	304050	1	AP004829 Staphyloc
C 3	826.4	87.3	307750	1	AP003136 Staphyloc
C 4	824.8	87.1	348550	1	AP003364 Staphyloc
C 5	369.8	39.0	306384	6	AX620460 Sequence
C 6	307	32.4	300698	1	AX5016750 Staphyloc
C 7	199.4	21.1	834	6	AX620416 Sequence
C 8	96.2	10.2	8056	6	AX599046 Sequence
C 9	92.8	9.8	170627	2	AC125567 Rattus no
C 10	91.4	9.7	67970	3	PFMAL1P3 Plasmodi
C 11	90.6	9.6	14422	3	AF466146 Melipona
C 12	90.4	9.5	86826	3	PFMAL3P5 Plasmodi
C 13	90	9.5	8056	6	AX599046 Sequence
C 14	87.6	9.3	258658	3	AX014832 Plasmodi
C 15	87.2	9.2	8056	6	AX598900 Sequence
C 16	85.2	9.0	286208	2	AC117140 Rattus no
C 17	85	9.0	840	8	CHS0180K Botrytis
C 18	84.8	9.0	2009	6	AX457067 Sequence
C 19	84.6	8.9	250029	3	AX014820 Plasmodi
C 20	84.2	8.9	259474	9	HUAC004605 Homo sapi
C 21	83.6	8.8	175544	2	AC117342 Rattus no
C 22	83	8.8	137411	9	AC092066 Homo sapi
C 23	82.8	8.7	1090	3	AB084761 Drosophila
C 24	82.8	8.7	169046	5	AL928828 Zebrafish
C 25	82.4	8.7	348600	1	AB063521 Wigglesworth
C 26	82.4	8.7	349980	6	AX344555 Sequence
C 27	82.2	8.7	196875	2	AC098095 Rattus no
C 28	82	8.7	6292	6	AX251493 Sequence
C 29	82	8.7	233877	9	AC093798 Homo sapi
C 30	81.6	8.6	349751	3	PFMAL4P3 Plasmodi
C 31	81.4	8.6	156040	2	AC004153 Plasmodi
C 32	81.4	8.6	250707	3	AE014848 Plasmodi
C 33	81.4	8.6	347050	3	PFAL929351 Plasmodi
C 34	81.2	8.6	99003	2	AL390756 Homo sapi
C 35	81.2	8.6	110000	2	PFMAL13_09 Continuation (10 o
C 36	81.2	8.6	318221	2	PFMAL13P3 Plasmodi
C 37	81	8.6	162445	9	AL158151 Human DNA
C 38	81	8.6	164640	2	BX005461 Danio rer
C 39	81	8.6	168558	2	BX322549 Danio rer
C 40	80.8	8.5	84563	5	AC096885 Danio rer
C 41	80.6	8.5	313050	3	PFAL929352 Plasmodi
C 42	80.2	8.5	8056	6	AX598900 Sequence
C 43	80.2	8.5	60604	2	AC023466 Homo sapi
C 44	80.2	8.5	181752	9	AC098822 Homo sapi
C 45	80	8.4	112695	8	AC119418 Medicago

ALIGNMENTS

RESULT 1
AF207701 947 bp DNA linear BCT 01-DEC-2000
Staphylococcus aureus putative transposase gene, partial cds; and
SarR (sarR) gene, complete cds.
AF207701
AF207701.1 GI:11493941
Staphylococcus aureus
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 947)
Cheung,A.L. and Manna,A.C.
Characterization of sarR, a modulator of sar expression in
Staphylococcus aureus

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 947)
AUTHORS Cheung A.L. and Manna, A.C.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-1999) Microbiology, Dartmouth Medical School,
College St., Hall 206, Hanover, NH 03755, USA
FEATURES
source
1..947
/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/strain="RM6390"
/db_xref="taxon:1280"
CDS
1..70
/codon_start=2
/transl_table=1
/product="putative transposase"
/protein_id="AGJ5716.1"
/db_xref="GI:11493943"
/translation="FSKSEVEHKEVHFLKIKYQ"
gene
208..555
/gene="sarR"
/notes="regulatory gene"
CDS
208..555
/gene="sarR"
/notes="similar to SarA"
/codon_start=1
/transl_table=1
/product="SarP"
/protein_id="AGJ5715.1"
/db_xref="GI:11493942"
/translation="MSKINDLVNATFQVKKFPRDTKKFNLYEIIYLNHLRS
SNEISSEKPAKSEFPYLTALQKLUKLSKSLQDERTVIVYVDTOKANI
OKUISEEYIKN"
BASE COUNT 374 a 112 c 145 g 316 t
ORIGIN
Query Match 100.0%; Score 947; DB 1; Length 947;
Best Local Similarity 100.0%; Pred. No. 7.7e-126;
Matches 947; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTTCAAAATCGGTGGAGTGCATCAAAAAGTTATTGGCATTTTGGCAATTTTGGAAATAAAA 60
DB 1 GTTTTCAAAATCGGTGGAGTGCATCAAAAAGTTATTGGCATTTTGGCAATTTTGGAAATAAAA 60
QY 61 ATATCAATAGTGGAGTGCATCAAAAAGTTATTGGCATTTTGGCAATTTTGGAAATAAAA 120
DB 61 ATATCAATAGTGGAGTGCATCAAAAAGTTATTGGCATTTTGGCAATTTTGGAAATAAAA 120
QY 121 TAACATAGTTGGATAGAGTTTTCGATTTAATACATTAATGTGAACCTTGCTACAACAAG 180
DB 121 TAACATAGTTGGATAGAGTTTTCGATTTAATACATTAATGTGAACCTTGCTACAACAAG 180
QY 181 ATGTGCATCAGAGGAGTGGTTTAAATAGTAAATTAATGTGAACCTTGCTACAACAAG 240
DB 181 ATGTGCATCAGAGGAGTGGTTTAAATAGTAAATTAATGTGAACCTTGCTACAACAAG 240
QY 241 AACGCAATTCAGTGAAGTGGTTTTCAGATACAAAAGAGTTCATTTGAAC 300
DB 241 AACGCAATTCAGTGAAGTGGTTTTCAGATACAAAAGAGTTCATTTGAAC 300
QY 301 TATGAAGAAATTTATTTTAAATCATATTTTAAAGAGTGCATTAACGAATCTCATCT 360
DB 301 TATGAAGAAATTTATTTTAAATCATATTTTAAAGAGTGCATTAACGAATCTCATCT 360
QY 361 AAAGAGATTGCTAGTCTCAGAGTTCAAACTTACTATTAACTAAAGCTTTTACAAG 420
DB 361 AAAGAGATTGCTAGTCTCAGAGTTCAAACTTACTATTAACTAAAGCTTTTACAAG 420
QY 421 CTAAGAGATTTAAATTTGTTATCAAGAAAGAGTTTCAAGACGAAGAGTATT 480
DB 421 CTAAGAGATTTAAATTTGTTATCAAGAAAGAGTTTCAAGACGAAGAGTATT 480
QY 481 GTTTATGTTACAGATACACAAAAGCAAAATTAACAAAATCTGATTTTCAAGATTAGAGAA 540

DB 481 GTTTATGTTACAGATACACAAAAGCAAAATTAACAAAATCTGATTTTCAAGATTAGAGAA 540
QY 541 TACATTAATAAATTAATCAAGGTAAATTTGGGTTTAAATAACATTGAACGATAACAATTTAT 600
DB 541 TACATTAATAAATTAATCAAGGTAAATTTGGGTTTAAATAACATTGAACGATAACAATTTAT 600
QY 601 TAATACGAAGTTATTTTACCATTCGGCATATAAATTAATTAATTAATTAATTAATTAATTA 660
DB 601 TAATACGAAGTTATTTTACCATTCGGCATATAAATTAATTAATTAATTAATTAATTAATTA 660
QY 661 AGATCGTTTAAATTAAGTTAAAGACCAACATACCTTATTTTCAAGCTTATTAAGCTTGCA 720
DB 661 AGATCGTTTAAATTAAGTTAAAGACCAACATACCTTATTTTCAAGCTTATTAAGCTTGCA 720
QY 721 CAAGTACACCTAGCTCTTTTATTTTAAATTAATTTTCTAGAAAATCAAGTTTACGATCAAA 780
DB 721 CAAGTACACCTAGCTCTTTTATTTTAAATTAATTTTCTAGAAAATCAAGTTTACGATCAAA 780
QY 781 ATATTTTCTGCGATATAGCTTTGGATGTTTCCCAAGTATTTTCTTATAATTTTGTGTGCGA 840
DB 781 ATATTTTCTGCGATATAGCTTTGGATGTTTCCCAAGTATTTTCTTATAATTTTGTGTGCGA 840
QY 841 TAAGCAAAATTTTACTGCAAAACCATGTGTAGGCAATTTGAGAAATAGCAACAGCAAA 900
DB 841 TAAGCAAAATTTTACTGCAAAACCATGTGTAGGCAATTTGAGAAATAGCAACAGCAAA 900
QY 901 TCGGATGTTATGCTATTAAGAACTAATGTTTTCATAACTGAATCGAT 947
DB 901 TCGGATGTTATGCTATTAAGAACTAATGTTTTCATAACTGAATCGAT 947
RESULT 2
AP004829/c 304050 bp DNA linear BCT 20-DEC-2002
LOCUS Staphylococcus aureus subsp. aureus MW2, complete genome,
strain:MW2, section 8/10.
ACCESSION AP004829 BA000033
VERSION AP004829.1 GI:121205117
KEYWORDS Staphylococcus aureus subsp. aureus MW2
SOURCE Staphylococcus aureus subsp. aureus MW2
ORGANISM Staphylococcus aureus subsp. aureus MW2
REFERENCE 1
AUTHORS Baba, T., Takeuchi, F., Kuroda, M., Yuzawa, H., Aoki, K., Oguchi, A.,
Nagai, Y., Iwama, N., Asano, K., Naimi, T., Kuroda, H., Cui, L.,
Yanamoto, K. and Hiramatsu, K.
Genome and virulence determinants of high virulence
community-acquired MRSA
Lancet 359 (9320), 1819-1827 (2002)
22040717
12044378
REFERENCE 2 (bases 1 to 304050)
AUTHORS Nagai, Y., Asano, K., Iwama, N., Baba, T., Kuroda, M., Hiramatsu, K. and
Kikuchi, H.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center, 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:bioelite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
FEATURES
source
1..304050
/organism="Staphylococcus aureus subsp. aureus MW2"
/mol_type="genomic DNA"
/strain="MW2"
/db_xref="taxon:196620"
gene complement(629..1072)
/gene="MW1947"
CDS complement(629..1072)
/gene="MW1947"
/note="ORFID:MW1947"

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: November 17, 2003, 09:13:34 ; Search time 316 Seconds
(without alignments)
8089.772 Million cell updates/sec

Title: US-10-043-539A-1

Perfect score: 947

Sequence: 1 gtttccaaatcgttgagg.....gtttccaaatcgaatcgat 947

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	34.7	400	18 AAV75836	Staphylococcus aur
2	261.4	27.6	387	24 AAV75836	Staphylococcus epi
3	96.2	10.2	8056	25 AB210246	Haematopoietic cel
4	90	9.5	8056	25 AB210246	Haematopoietic cel
5	87.2	9.2	8056	25 AB210100	Haematopoietic cel
6	82	8.7	6292	22 AAS46735	Tumour suppressor
7	80.2	8.5	8056	25 AB210100	Haematopoietic cel.
8	79.4	8.4	101	18 AAV75910	Staphylococcus aur

C 9	77.6	8.2	867	24	ABN92692	Staphylococcus epi
C 10	75.6	8.0	529	21	AA365121	E. coli proliferat
C 11	75.2	7.9	12078	24	ABQ76793	pUC19 promoter-ter
C 12	75.2	7.9	12078	24	ABV74271	Plant specific exp
C 13	75.2	7.9	12085	24	ABQ76792	pUC19 promoter-ter
C 14	75.2	7.9	12085	24	ABQ76792	Plant specific exp
C 15	75.2	7.9	12093	24	ABQ76791	pUC19 promoter-ter
C 16	75.2	7.9	12093	24	ABQ76791	Plant specific exp
C 17	75.2	7.9	12241	24	ABQ73049	Tomato anthocyanin
C 18	75.2	7.9	12241	24	AA365121	Binary vector DNA
C 19	75.2	7.9	13002	24	ABQ76794	pUC19 promoter-ter
C 20	75.2	7.9	13002	24	ABQ76794	Plant specific exp
C 21	75.2	7.9	13737	21	AA54212	Transformation vec
C 22	75.2	7.9	13905	24	ABQ76795	pUC19 promoter-ter
C 23	75.2	7.9	13905	24	ABQ76795	Plant specific exp
C 24	75.2	7.9	14446	24	AA365121	Plasmid pTM036
C 25	75.2	7.9	15430	24	ABQ76796	Plant specific exp
C 26	75.2	7.9	15430	24	ABQ76796	Plant specific exp
C 27	75.2	7.9	17752	24	ABQ76797	Plant specific exp
C 28	75.2	7.9	17752	24	ABQ76797	Plant specific exp
C 29	75.2	7.9	19705	24	AA92074	Vector plasmid pBT
C 30	75.2	7.9	20119	22	AAH26041	Plasmid pNOV524 en
C 31	75.2	7.9	20174	24	AAH26041	Transformation vec
C 32	75.2	7.9	26019	22	AAH26040	Plasmid pNOV523 en
C 33	75	7.9	6664	24	AAH26040	Human gene regulat
C 34	74.6	7.9	4086	22	AAH54401	S. epidermidis gen
C 35	74.4	7.9	778	24	ABQ15588	Oligonucleotide fo
C 36	74.4	7.9	778	24	ABQ15588	Human chemically m
C 37	73.2	7.7	6191	24	ABN80161	Human immune syste
C 38	73.2	7.7	6191	24	ABL70282	Chemically treated
C 39	73.2	7.7	6191	24	ABL70282	Signal transductio
C 40	73.2	7.7	6191	24	ABL331307	Human immune syste
C 41	73.2	7.7	15548	24	ABL34155	Human immune syste
C 42	72.2	7.6	3967	22	AAH54106	S. epidermidis gen
C 43	72	7.6	1501	25	AB210198	Haematopoietic cel
C 44	72	7.6	2145	21	AA256364	Escherichia coli f
C 45	72	7.6	4142	22	AAH54879	S. epidermidis gen

ALIGNMENTS

RESULT 1

AAV75836
ID AAV75836 standard; DNA; 400 BP.

XX

XX

AC AAV75836;

XX

DT 16-MAR-1999 (first entry)

XX

DE Staphylococcus aureus contig SEQ ID #1525.

XX

KW Computer readable medium; vaccine; S. aureus infection; immunodetection;

KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KW skin infection; surgical wound infection; scalded skin syndrome;

KW toxic shock syndrome; ds.

XX

OS Staphylococcus aureus.

XX

XX

FT Key

FT misc_feature

FT Location/Qualifiers

FT 301..360

FT /*tag= a

FT /notes

FT

FT

FT

FT

FT

FT

FT

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

These bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

EP786519-A2.

30-JUL-1997.

07-JAN-1997; 97EP-0100117.

